SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT:
        (A) NAME: The University of Leicester
        (B) STREET: University Road
        (C) CITY: Leicester
        (E) COUNTRY: United Kingdom
        (F) POSTAL CODE (ZIP): LE1 7RH

    (ii) TITLE OF INVENTION: Complement Inhibitor

   (iii) NUMBER OF SEQUENCES: 14

    (iv) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(2) INFORMATION FOR SEQ ID NO: 1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 4229 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

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TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC      60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT     120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT     180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG     240

AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG     300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG     360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTGAATGTG     420

ATGCAGATGG GTGGACCAAT GATATTCCAA TATGTGAAGT TGTGAAGTGC TTGCCAGTGA     480

CAGAACTGGA GAATGGAAGA ATTGTGAGTG GTGCAGCCGA ACCAGACCAG GAATATTATT     540

TTGGACAGGT GGTACGCTTT GAATGCAACT CCGGCTTCAA GATTGAAGGA CAGAAAGAAA     600

TGCACTGCTC ATAAAATGGC CTCTGGAGCA ATGAAAAGCC ACAGTGTGTG GAAATTTCTT     660
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GCCTGCCACC ACGAGTTGAA AATGGAGATG GTATATATCT GAAACCAGTT TACAAGGAGA    720

ATGAAAGATT CCAATATAAA TGTAAGCAAG GTTTTGTGTA CAAAGAAAGA GGGGATGCTG    780

TCTGCACGGG TTCTGGATGG AATCCTCAGC CTTCCTGTGA AGAAATGACA TGTTTGACTC    840

CATATATTCC AAATGGTATC TACACACCTC ACAGGATTAA ACACAGAATT GATGATGAAA    900

TCAGATATGA ATGTAAAAAT GGCTTCTATC CTGCAACCCG ATCACCTGTT TCAAAGTGTA    960

CAATTACTGG CTGGATCCCT GCTCCAAGAT GTAGCTTGAA ACCTTGTGAT TTTCCACAAT   1020

TCAAACATGG ACGTCTGTAT TATGAAGAAA GCCGGAGACC CTACTTCCCA GTACCTATAG   1080

GAAAGGAGTA CAGCTATAAC TGTGACAACG GGTTTACAAC GCCTTCACAG TCATACTGGG   1140

ACTACCTTCG TTGCACAGTA AATGGGTGGG AGCCTGAAGT TCCATGCCTC AGGCAATGTA   1200

TTTTCCATTA TGTGGAATAT GGAGAATCTT CATACTGGCA AGAAGATAT ATAGAGGGTC   1260

AGTCTGCAAA AGTCCAGTGT CACAGTGGCT ATAGTCTTCC AAATGGTCAA GATACATATT   1320

ATTGTACAGA GAATGGCTGG TCCCCTCCTC CCAAATGCGT CCGTATCAAG ACTTGTTCAG   1380

TATCAGATAT AGAAATTGAA AATGGGTTTT TTTCTGAATC TGATTATACA TATGCTCTAA   1440

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GAATAATTAC TTGTCTTCAA GATGGATGGT CACCTCGACC CTCATGCATT AAGTCTTGTG   1560

ATATGCCTGT ATTTGAGAAT TCTATGACTA AGAATAATAA CACATGGTTT AAACTCAATG   1620

ACAAATTAGA CTATGAATGT CACATTGGAT ATGAAAATGA ATATAAACAT ACCAAAGGCT   1680

CTATAACATG TACTTATGAT GGATGGTCTA GTACACCTC CTGTTATGAA AGAGAATGCA   1740

GCATTCCCCT GTTACACCAA GACTTAGTTG TTTTTCCCAG AGAAGTAAAA TACAAAGTTG   1800

GAGATTCGTT GAGTTTCTCT TGCCGTTCAG GACACAGAGT TGGAGCAGAT TTAGTGCAAT   1860

GCTACCACTT TGGATGGTCC CCTAATTTCC CAACGTGTGA AGGCCAAGTA AAATCATGTG   1920

ACCAACCTCT TGAAATCCCG AATGGGGAAA TAAAGGGAAC AAAAAAAGTT GAATACAGCC   1980

ATGGTGACGT GGTGGAATAT GATTGCAAAC CTAGATTTCT ACTGAAGGGA CCCAATAAAA   2040

TCCAGTGTGT TGACGGGAAG TGGACAAGGT TGCCGATATG CGTTGAGTAT GAGAGAACAT   2100

GTGGAGACCT TCCTGAACTT GAGCATGGCT CTGTCAAGTT ATCTGTCCCT CCCTACCATC   2160

ATGGAGATTC AGTGGAGTTC ACTTGTACAG AAACCTTCAC AATGATTGGA CATGCAGTAG   2220

TTTTCTGCAT TAGTGGAAGG TGGACCGAGC TTCCTCAATG TGTTGCAACA GATCAACTGG   2280

AGAAGTGTAA AGCCCCGAAG TCAACTGGCA TAGATGCAAT TCATCCAAAT AAGAATGAAT   2340
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TTAATCATAA CTTTAGTGTG AGTTACAGAT GTAGACAAAA GCAGGAGTAT GAACATTCAA    2400

TCTGCATCAA TGGAAGATGG GATCCTGAAC CAAACTGTAC AAGCAAAAGA TTCTGCCCTC    2460

CTCCCCCGCA GATTCCAAAT GCCCAAGTGA TTGAAACCAC CGTGAAATAC TTGGATGGAG    2520

AAAAAGTATC TGTTCTTTGC CAAGATGGTT ACCTAACTCA GGGCCCAGAA GAAATGGTGT    2580

GTAAACATGG AAGGTGGCAG TCGTTACCAC GCTGCACGGA AAAAATTCCA TGTTCCCAGC    2640

CCCCTAAAAT TGAACATGGA TCTATTAAGT CGCCCAGGTC CTCAGAAGAG AGGAGAGATT    2700

TAATTGAGTC CAGCAGTTAT GAACACGGAA CTACATTCAG CTATTGCTGT AGAGATGGAT    2760

TCAAGATATC TGAAGAAAAT AGGGTAACCT GCAACATGGG AAAATGGAGC TCTCTGCCTC    2820

GTTGTGTTGG AATACCTTGT GGACCCCCAC CTTCAATTCC TCTTGGTATT GTTTCTCATG    2880

AACTAGAAAG TTACCAATAT GGAGAGGAGG TTACATACAA TTGTTCTGAA GGCTTTGGAA    2940

TTGATGGACC AGCATTTATT AAATGTGTAG GAGGACAGTG GTCTGAACCT CCCAAATGCA    3000

TAAAAACTGA TTGTGACAAC TTGCCCACAT TTGAAATTGC CAAACCGACA GAAAAGAAAA    3060

AAAAATCATA CAGGTCAGGA GAACAAGTGA CATTCAGATG TCCACCTCCG TATCGAATGG    3120

ATGGCTCTGA CATTGTCACA TGTGTTAATA CGAAGTGGAT TGGACAGCCG GTATGCAAAG    3180

ATAATTCCTG TGTGAATCCA CCACATGTGC CAAATGCTAC TATACTAACA AGGCACAAGA    3240

CTAAATATCC ATCTGGTGAC AAAGTACGTT ATGACTGTAA TAAACCTTTT GAATTATTTG    3300

GGGAAGTGGA AGTGATGTGC CAAAACGGGA TTTGGACAGA ACCACCGAAA TGCAAAGATT    3360

CAACAGGGAA ATGTGGGCCT CCTCCACCTA TTGACAATGG AGACATCACC TCCTTGTCAT    3420

TACCAGTATA TGCACCATTA TCATCAGTTG AATATCAATG CCAGAACTAT TATCTACTTA    3480

AGGGAAATAA GATAGTAACA TGTAGAAATG GAAAGTGGTC TCAGCCACCA ACCTGCTTAC    3540

ATGCATGTGT GATACCAGAA GATATTATGG AAAAACATAA TATAGTTCTC AGATGGAGGG    3600

AAAATGCAAA GATTTATTCC CAATCAGGGG AGAATATTGA ATTCATGTGT AAACCTGGAT    3660

ATAGAAAATT CAGAGGATCA CCTCCGTTTC GTACAAAGTG CATTGAGGGT CACATCAATT    3720

ATCCCACTTG TGTATAAAAT CGCTATACAA TTATTAGTAA ACCTTATGGA TGAGAAATGC    3780

ACATGTATAT TACTAATACA GTTTGAATTT ACATTTAAAT ATTGTTTAGC TCATTTCCTC    3840

TAATAAGTAT ATAAACTTTT TTTATATGGT GGTTAATCAG TAACTTTACA GACTGTTGCC    3900

ACAAAGCAAG AACATTACAT TCAAAACTCC TAATCCAAAT ATGATATGTC CAAGGACAAA    3960

CTATGTCTAA GCAAGAAAAT AAATGTTAGT TCTTCAATGT CTGTTTTTAT TCAGGACCTT    4020
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TCAGATTTTC TTGGATACCT TTTGTTAGGT TCTGATTCAC AGTGAGTGGA AGACACACTG   4080

ACTCTGACTT CAAATTAGTA TTACTTGCAA TACATTAACA ACCAAACTAT CATAATATCA   4140

CAAATGTATA CAGCTAATTA CTGTGTCCTA CCTTTGTATC AATAAAGAAA TCTAAGAAAG   4200

TTCTTGCTTA AAAAAAAAAA AAAAAAAAA   4229

(2) INFORMATION FOR SEQ ID NO: 2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 866 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC   60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT   120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT   180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG   240

AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG   300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG   360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTGAATGTG   420

ATGCAGATGG GTGGACCAAT GATATTCCAA TATGTGAAGT TGTGAAGTGC TTGCCAGTGA   480

CAGAACTGGA GAATGGAAGA ATTGTGAGTG GTGCAGCCGA ACCAGACCAG GAATATTATT   540

TTGGACAGGT GGTACGCTTT GAATGCAACT CCGGCTTCAA GATTGAAGGA CAGAAAGAAA   600

TGCACTGCTC ATAAAATGGC CTCTGGAGCA ATGAAAAGCC ACAGTGTGTG GAAATTTCTT   660

GCCTGCCACC ACGAGTTGAA AATGGAGATG GATATAGAAA ATTCAGAGGA TCACCTCCGT   720

TTCGTACAAA GTGCATTGAG GGTCACATCA ATTATCCCAC TTGTGTATAA AATCGCTATA   780

CAATTATTAG TAAACCTTAT GGATGACACT TTGTTTAGAA ATGCACATGT ATATTACTAA   840

TACAGTTTGA ATTTACATTT GAAAAA   866

(2) INFORMATION FOR SEQ ID NO: 3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 2715 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

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TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC      60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT     120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT     180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG     240

AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG     300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG     360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTGAATGTG     420

ATGCAGATGG GTGGACCAAT GATATTCCAA TATGTGAAGT TGTGAAGTGC TTGCCAGTGA     480

CAGAACTGGA GAATGGAAGA ATTGTGAGTG GTGCAGCCGA ACCAGACCAG GAATATTATT     540

TTGGACAGGT GGTACGCTTT GAATGCAACT CCGGCTTCAA GATTGAAGGA CAGAAAGAAA     600

TGCACTGCTC ATAAAATGGC CTCTGGAGCA ATGAAAGCC ACAGTGTGTG TTGAAACCTT     660

GTGATTTTCC ACAATTCAAA CATGGACGTC TGTATTATGA AGAAAGCCGG AGACCCTACT     720

TCCCAGTACC TATAGGAAAG GAGTACAGCT ATAACTGTGA CAACGGGTTT ACAACGCCTT     780

CACAGTCATA CTGGGACTAC CTTCGTTGCA CAGTAAATGG GTGGGAGCCT GAAGTTCCAT     840

GCCTCAGGCA ATGTATTTTC CATTATGTGG AATATGGAGA ATCTTCATAC TGGCAAAGAA     900

GATATATAGA GGGTCAGTCT GCAAAAGTCC AGTGTCACAG TGGCTATAGT CTTCCAAATG     960

GTCAAGATAC ATATTATTGT ACAGAGAATG GCTGGTCCCC TCCTCCCAAA TGCGTCCGTA    1020

TCAAGACTTG TTCAGTATCA GATATAGAAA TTGAAAATGG GTTTTTTTCT GAATCTGATT    1080

ATACATATGC TCTAAATAGA AAAACACGGT ATAGATGTAA ACAGGGATAT GTAACAAATA    1140

CCGGAGAAAT ATCAGGAATA ATTACTTGTC TTCAAGATGG ATGGTCACCT CGACCCTCAT    1200

GCATTAAGTC TTGTGATATG CCTGTATTTG AGAATTCTAT GACTAAGAAT AATAACACAT    1260

GGTTTAAACT CAATGACAAA TTAGACTATG AATGTCACAT GGATATGAA AATGAATATA    1320

AACATACCAA AGGCTCTATA ACATGTACTT ATGATGGATG GTCTAGTACA CCCTCCTGTT    1380

ATGAAAGAGA ATGCAGCATT CCCCTGTTAC ACCAAGACTT AGTTGTTTTT CCCAGAGAAG    1440

TAAAATACAA AGTTGGAGAT TCGTTGAGTT TCTCTTGCCG TTCAGGACAC AGAGTTGGAG    1500

CAGATTTAGT GCAATGCTAC CACTTTGGAT GGTCCCCTAA TTTCCCAACG TGTGAAGGCC    1560

AAGTAAAATC ATGTGACCAA CCTCTTGAAA TCCCGAATGG GGAAATAAAG GGAACAAAAA    1620
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AAGTTGAATA CAGCCATGGT GACGTGGTGG AATATGATTG CAAACCTAGA TTTCTACTGA   1680

AGGGACCCAA TAAAATCCAG TGTGTTGACG GGAAGTGGAC AAGGTTGCCG ATATGCGTTG   1740

AGTATGAGAG AACATGTGGA GACCTTCCTG AACTTGAGCA TGGCTCTGTC AAGTTATCTG   1800

TCCCTCCCTA CCATCATGGA GATTCAGTGG AGTTCACTTG TACAGAAACC TTCACAATGA   1860

TTGGACATGC AGTAGTTTTC TGCATTAGTG GAAGGTGGAC CGAGCTTCCT CAATGTGTTG   1920

CAACAGATCA ACTGGAGAAG TGTAAAGCCC CGAAGTCAAC TGGCATAGAT GCAATTCATC   1980

CAAATAAGAA TGAATTTAAT CATAACTTTA GTGTGAGTTA CAGATGTAGA CAAAAGCAGG   2040

AGTATGAACA TTCAATCTGC ATCAATGGAA GATGGGATCC TGAACCAAAC TGTACAAGCA   2100

AAAGATTCTG CCCTCCTCCC CCGCAGATTC CAAATGCCCA AGTGATTGAA ACCACCGTGA   2160

AATACTTGGA TGGAGAAAAA GTATCTGTTC TTTGCCAAGA TGGTTACCTA ACTCAGGGCC   2220

CAGAAGAAAT GGTGTGTAAA CATGGAAGGT GGCAGTCGTT ACCACGCTGC ACGGAAAAAA   2280

TTCCATGTTC CCAGCCCCCT AAAATTGAAC ATGGATCTAT TAAGTCGCCC AGGTCCTCAG   2340

AAGAGAGGAG AGATTTAATT GAGTCCAGCA GTTATGAACA CGGAACTACA TTCAGCTATT   2400

GCTGTAGAGA TGGATTCAAG ATATCTGAAG AAAATAGGGT AACCTGCAAC ATGGGAAAAT   2460

GGAGCTCTCT GCCTCGTTGT GTTGGAATAC CTTGTGGACC CCCACCTTCA ATTCCTCTTG   2520

GTATTGTTTC TCATGAACTA GAAAGTTACC AATATGGAGA GGAGGTTACA TACAATTGTT   2580

CTGAAGGCTT TGGAATTGAT GGACCAGCAT TTATTAAATG TGTAGGAGGA CAGTGGTCTG   2640

AACCTCCCAA ATGCATAAAA ACTGATTGTG CAACTTGCC CACATTGAA ATTGCCAAAC   2700

CGACAGAAAA GAAAA   2715

(2) INFORMATION FOR SEQ ID NO: 4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 1532 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: double
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

TCGAGTCAAC TGCTCCCAGA TAGATCCAAG ACATGAGACT GTCAGCAAGA ATTATTTGGC   60

TTATATTATG GACTGTTTGT GTAGCAGAAG ATTGTAAAGG TCCTCCTCCA AGAGAAAATT   120

CAGAAATTCT CTCAGGTTCG TGGTCTGAAC AACTATATTC AGAAGGCACT CAGGCAACCT   180

ACAAATGCCG CCCTGGATAC CGAACACTTG GTACTATTGT AAAAGTATGC AAGAATGGAG   240

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AATGGGTACC TTCTAACCCA TCAAGGATAT GTCGGAAAAG GCCATGTGGG CATCCCGGAG    300

ACACACCCTT TGGGTCCTTT AGGCTGGCAG TTGGATCTGA ATTTGAATTT GGTGCAAAGG    360

TTGTTTATAC ATGTGATGAA GGGTACCAAC TATTAGGTGA AATTGATTAC CGTTATCGAA    420

TGGATGGCTC TGACATTGTC ACATGTGTTA ATACGAAGTG GATTGGACAG CCGGTATGCA    480

AAGATAATTC CTGTGTGAAT CCACCACATG TGCCAAATGC TACTATACTA ACAAGGCACA    540

AGACTAAATA TCCATCTGGT GACAAAGTAC GTTATGACTG TAATAAACCT TTTGAATTAT    600

TTGGGGAAGT GGAAGTGATG TGCCAAAACG GGATTTGGAC AGAACCACCG AAATGCAAAG    660

ATTCAACAGG GAAATGTGGG CCTCCTCCAC CTATTGACAA TGGAGACATC ACCTCCTTGT    720

CATTACCAGT ATATGCACCA TTATCATCAG TTGAATATCA ATGCCAGAAC TATTATCTAC    780

TTAAGGGAAA TAAGATAGTA ACATGTAGAA ATGGAAAGTG GTCTCAGCCA CCAACCTGCT    840

TACATGCATG TGTGATACCA GAAGATATTA TGGAAAAACA TAATATAGTT CTCAGATGGA    900

GGGAAAATGC AAAGATTTAT TCCCAATCAG GGAGAATAT TGAATTCATG TGTAAACCTG    960

GATATAGAAA ATTCAGAGGA TCACCTCCGT TTCGTACAAA GTGCATTGAG GGTCACATCA   1020

ATTATCCCAC TTGTGTATAA AATCGCTATA CAATTATTAG TAAACCTTAT GGATGAGAAA   1080

TGCACATGTA TATTACTAAT ACAGTTTGAA TTTACATTTA AATATTGTTT AGCTCATTTC   1140

CTCTAATAAG TATATAAACT TTTTTATAT GGTGGTTAAT CAGTAACTTT ACAGACTGTT   1200

GCCACAAAGC AAGAACATTA CATTCAAAAC TCCTAATCCA AATATGATAT GTCCAAGGAC   1260

AAACTATGTC TAAGCAAGAA AATAAATGTT AGTTCTTCAA TGTCTGTTTT TATTCAGGAC   1320

CTTTCAGATT TTCTTGGATA CCTTTTGTTA GGTTCTGATT CACAGTGAGT GGAAGACACA   1380

CTGACTCTGA CTTCAAATTA GTATTACTTG CAATACATTA ACAACCAAAC TATCATAATA   1440

TCACAAATGT ATACAGCTAA TTACTGTGTC CTACCTTTGT ATCAATAAAG AAATCTAAGA   1500

AAGTTCTTGC TTAAAAAAAA AAAAAAAAAA AA                                 1532
```

(2) INFORMATION FOR SEQ ID NO: 5:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TTCAAGTAAC GTTAGAAGCT TAAGATG   27

(2) INFORMATION FOR SEQ ID NO: 6:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 33 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: unknown

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GGCGGCCGCT CAAATCTTCT GAGATATAGG AGA   33

(2) INFORMATION FOR SEQ ID NO: 7:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 33 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: unknown

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGCGGCCGCT CATTTAATCC TTAAAGGTGA GTA   33

(2) INFORMATION FOR SEQ ID NO: 8:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 33 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: unknown

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GGCGGCCGCT CATACTGGAA AGTATGGTCT ACG   33

(2) INFORMATION FOR SEQ ID NO: 9:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 207 amino acids
             (B) TYPE: amino acid
             (C) STRANDEDNESS:
             (D) TOPOLOGY: unknown

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

        Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
        1   5   10   15

        Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
                        20   25   30

```
Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
         35              40              45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
     50              55              60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65              70              75                      80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
                 85              90                  95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
             100             105             110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
             115             120             125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
         130             135             140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145             150             155             160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
             165             170             175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
             180             185             190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile
         195             200             205
```

(2) INFORMATION FOR SEQ ID NO: 10:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 265 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

```
Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1               5               10              15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
             20              25              30

Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
         35              40              45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
     50              55              60
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Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65            70            75            80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
              85            90            95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
              100           105           110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
              115           120           125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
    130           135           140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145           150           155           160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
              165           170           175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
              180           185           190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
    195           200           205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
210           215           220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225           230           235           240

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn
              245           250           255

Gly Asp Tyr Ser Pro Leu Arg Ile Lys
              260           265
```

(2) INFORMATION FOR SEQ ID NO: 11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 329 amino acids
        (B) TYPE: amino acid
        (C) STRANDEDNESS:
        (D) TOPOLOGY: unknown

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

```
Glu Asp Cys Asn Glu Leu Pro Pro Arg Arg Asn Thr Glu Ile Leu Thr
1             5             10            15

Gly Ser Trp Ser Asp Gln Thr Tyr Pro Glu Gly Thr Gln Ala Ile Tyr
    20            25            30
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Lys Cys Arg Pro Gly Tyr Arg Ser Leu Gly Asn Val Ile Met Val Cys
         35                  40                  45

Arg Lys Gly Glu Trp Val Ala Leu Asn Pro Leu Arg Lys Cys Gln Lys
         50              55                  60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Thr Phe Thr Leu
65                      70              75                      80

Thr Gly Gly Asn Val Phe Glu Tyr Gly Val Lys Ala Val Tyr Thr Cys
                 85                  90                  95

Asn Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asn Tyr Arg Glu Cys Asp
             100                 105                 110

Thr Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
             115                 120                 125

Leu Pro Val Thr Ala Pro Glu Asn Gly Lys Ile Val Ser Ser Ala Met
         130                 135                 140

Glu Pro Asp Arg Glu Tyr His Phe Gly Gln Ala Val Arg Phe Val Cys
145                 150                 155                 160

Asn Ser Gly Tyr Lys Ile Glu Gly Asp Glu Glu Met His Cys Ser Asp
                 165                 170                 175

Asp Gly Phe Trp Ser Lys Glu Lys Pro Lys Cys Val Glu Ile Ser Cys
             180                 185                 190

Lys Ser Pro Asp Val Ile Asn Gly Ser Pro Ile Ser Gln Lys Ile Ile
         195                 200                 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Asn Met Gly Tyr Glu
         210                 215                 220

Tyr Ser Glu Arg Gly Asp Ala Val Cys Thr Glu Ser Gly Trp Arg Pro
225                 230                 235                 240

Leu Pro Ser Cys Glu Glu Lys Ser Cys Asp Asn Pro Tyr Ile Pro Asn
                 245                 250                 255

Gly Asp Tyr Ser Pro Leu Arg Ile Lys His Arg Thr Gly Asp Glu Ile
             260                 265                 270

Thr Tyr Gln Cys Arg Asn Gly Phe Tyr Pro Ala Thr Arg Gly Asn Thr
             275                 280                 285

Ala Lys Cys Thr Ser Thr Gly Trp Ile Pro Ala Pro Arg Cys Thr Leu
         290                 295                 300

Lys Pro Cys Asp Tyr Pro Asp Ile Lys His Gly Gly Leu Tyr His Glu
305                 310                 315                 320

Asn Met Arg Arg Pro Tyr Phe Pro Val
                 325
```

(2) INFORMATION FOR SEQ ID NO: 12:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 32 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

CCTCCTCCTG GAAATGTTAG AAGCTTAAGA TG   32

(2) INFORMATION FOR SEQ ID NO: 13:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 29 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: single
          (D) TOPOLOGY: unknown

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCTCTAGATT ACTTGATACG GACGCATTT   29

(2) INFORMATION FOR SEQ ID NO: 14:

     (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 428 amino acids
          (B) TYPE: amino acid
          (C) STRANDEDNESS:
          (D) TOPOLOGY: unknown

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Glu Asp Cys Lys Gly Pro Pro Pro Arg Glu Asn Ser Glu Ile Leu Ser
1   5   10   15

Gly Ser Trp Ser Glu Gln Leu Tyr Ser Glu Gly Thr Gln Ala Thr Tyr
            20   25   30

Lys Cys Arg Pro Gly Tyr Arg Thr Leu Gly Thr Ile Val Lys Val Cys
        35   40   45

Lys Asn Gly Glu Trp Val Pro Ser Asn Pro Ser Arg Ile Cys Arg Lys
    50   55   60

Arg Pro Cys Gly His Pro Gly Asp Thr Pro Phe Gly Ser Phe Arg Leu
65   70   75   80

Ala Val Gly Ser Glu Phe Glu Phe Gly Ala Lys Val Val Tyr Thr Cys
                85   90   95

Asp Glu Gly Tyr Gln Leu Leu Gly Glu Ile Asp Tyr Arg Glu Cys Asp

```
                100                    105                    110
Ala Asp Gly Trp Thr Asn Asp Ile Pro Ile Cys Glu Val Val Lys Cys
        115                 120                 125

Leu Pro Val Thr Glu Leu Glu Asn Gly Arg Ile Val Ser Gly Ala Ala
        130                 135                 140

Glu Pro Asp Gln Glu Tyr Tyr Phe Gly Gln Val Val Arg Phe Glu Cys
145                 150                 155                 160

Asn Ser Gly Phe Lys Ile Glu Gly Gln Lys Glu Met His Cys Ser Glu
                165                 170                 175

Asn Gly Leu Trp Ser Asn Glu Lys Pro Gln Cys Val Glu Ile Ser Cys
                180                 185                 190

Leu Pro Pro Arg Val Glu Asn Gly Asp Gly Ile Tyr Leu Lys Pro Val
                195                 200                 205

Tyr Lys Glu Asn Glu Arg Phe Gln Tyr Lys Cys Lys Gln Gly Phe Val
        210                 215                 220

Tyr Lys Glu Arg Gly Asp Ala Val Cys Thr Gly Ser Gly Trp Asn Pro
225                 230                 235                 240

Gln Pro Ser Cys Glu Glu Met Thr Cys Leu Thr Pro Tyr Ile Pro Asn
                245                 250                 255

Gly Ile Tyr Thr Pro His Arg Ile Lys His Arg Ile Asp Asp Glu Ile
                260                 265                 270

Arg Tyr Glu Cys Lys Asn Gly Phe Tyr Pro Ala Thr Arg Ser Pro Val
        275                 280                 285

Ser Lys Cys Thr Ile Thr Gly Trp Ile Pro Ala Pro Arg Cys Ser Leu
        290                 295                 300

Lys Pro Cys Asp Phe Pro Gln Phe Lys His Gly Arg Leu Tyr Tyr Glu
305                 310                 315                 320

Glu Ser Arg Arg Pro Tyr Phe Pro Val Pro Ile Gly Lys Glu Tyr Ser
                325                 330                 335

Tyr Tyr Cys Asp Asn Gly Phe Thr Thr Pro Ser Gln Ser Tyr Trp Asp
                340                 345                 350

Tyr Leu Arg Cys Thr Val Asn Gly Trp Glu Pro Glu Val Pro Cys Leu
        355                 360                 365

Arg Gln Cys Ile Phe His Tyr Val Glu Tyr Gly Glu Ser Ser Tyr Trp
        370                 375                 380

Gln Arg Arg Tyr Ile Glu Gly Gln Ser Ala Lys Val Gln Cys His Ser
385                 390                 395                 400
```

```
Gly Tyr Ser Leu Pro Asn Gly Gln Asp Thr Tyr Tyr Cys Thr Glu Asn
                405                 410                 415

Gly Trp Ser Pro Pro Pro Lys Cys Val Arg Ile Lys
                420             425
```

Figure 1

```
            10        20        30 -18     40        50        60
tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC    rFH4.3
tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC    rFH2.7
tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC    rFH1.8
tcgagtcaactgctcccagatagatccaagacATGAGACTGTCAGCAAGAATTATTTGGC    rFH1.0


                                  SCR1
            70        80       +1 90       100       110       120
TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT    rFH4.3
TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT    rFH2.7
TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT    rFH1.8
TTATATTATGGACTGTTTGTGTAGCAGAAGATTGTAAAGGTCCTCCTCCAAGAGAAAATT    rFH1.0


            130       140       150       160       170       180
CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT    rFH4.3
CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT    rFH2.7
CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT    rFH1.8
CAGAAATTCTCTCAGGTTCGTGGTCTGAACAACTATATTCAGAAGGCACTCAGGCAACCT    rFH1.0


            190       200       210       220       230       240
ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG    rFH4.3
ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG    rFH2.7
ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG    rFH1.8
ACAAATGCCGCCCTGGATACCGAACACTTGGTACTATTGTAAAAGTATGCAAGAATGGAG    rFH1.0


                                  SCR2a
            250       260       270       280       290       300
AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG    rFH4.3
AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG    rFH2.7
AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG    rFH1.8
AATGGGTACCTTCTAACCCATCAAGGATATGTCGGAAAAGGCCATGTGGGCATCCCGGAG    rFH1.0


            310       320       330       340       350       360
ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG    rFH4.3
ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG    rFH2.7
ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG    rFH1.8
ACACACCCTTTGGGTCCTTTAGGCTGGCAGTTGGATCTGAATTTGAATTTGGTGCAAAGG    rFH1.0
```

```
                 SCR2b
     370       380       390       400       410       420
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGTGAATGTG     rFH4.3
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGTGAATGTG     rFH2.7
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGT-------     rFH1.8
TTGTTTATACATGTGATGAAGGGTACCAACTATTAGGTGAAATTGATTACCGTGAATGTG     rFH1.0


                                  SCR3
     430       440       450       460       470       480
ATGCAGATGGGTGGACCAATGATATTCCAATATGTGAAGTTGTGAAGTGCTTGCCAGTGA     rFH4.3
ATGCAGATGGGTGGACCAATGATATTCCAATATGTGAAGTTGTGAAGTGCTTGCCAGTGA     rFH2.7
------------------------------------------------------------     rFH1.8
ATGCAGATGGGTGGACCAATGATATTCCAATATGTGAAGTTGTGAAGTGCTTGCCAGTGA     rFH1.0


     490       500       510       520       530       540
CAGAACTGGAGAATGGAAGAATTGTGAGTGGTGCAGCCGAACCAGACCAGGAATATTATT     rFH4.3
CAGAACTGGAGAATGGAAGAATTGTGAGTGGTGCAGCCGAACCAGACCAGGAATATTATT     rFH2.7
------------------------------------------------------------     rFH1.8
CAGAACTGGAGAATGGAAGAATTGTGAGTGGTGCAGCCGAACCAGACCAGGAATATTATT     rFH1.0


     550       560       570       580       590       600
TTGGACAGGTGGTACGCTTTGAATGCAACTCCGGCTTCAAGATTGAAGGACAGAAAGAAA     rFH4.3
TTGGACAGGTGGTACGCTTTGAATGCAACTCCGGCTTCAAGATTGAAGGACAGAAAGAAA     rFH2.7
------------------------------------------------------------     rFH1.8
TTGGACAGGTGGTACGCTTTGAATGCAACTCCGGCTTCAAGATTGAAGGACAGAAAGAAA     rFH1.0


                                              SCR4
     610       620       630       640       650       660
TGCACTGCTCATAAAATGGCCTCTGGAGCAATGAAAAGCCACAGTGTGTGGAAATTTCTT     rFH4.3
TGCACTGCTCATAAAATGGCCTCTGGAGCAATGAAAAGCCACAGTGTGTG----------     rFH2.7
------------------------------------------------------------     rFH1.8
TGCACTGCTCATAAAATGGCCTCTGGAGCAATGAAAAGCCACAGTGTGTGGAAATTTCTT     rFH1.0


     670       680       690       700       710       720
GCCTGCCACCACGAGTTGAAAATGGAGATGGTATATATCTGAAACCAGTTTACAAGGAGA     rFH4.3
------------------------------------------------------------     rFH2.7
------------------------------------------------------------     rFH1.8
GCCTGCCACCACGAGTTGAAAATGGAGAT-------------------------------     rFH1.0
```

```
            730       740       750       760       770       780
ATGAAAGATTCCAATATAAATGTAAGCAAGGTTTTGTGTACAAAGAAAGAGGGGATGCTG   rFH4.3
-----------------------------------------------------------   rFH2.7
-----------------------------------------------------------   rFH1.8
-----------------------------------------------------------   rFH1.0


                                        SCR5
            790       800       810       820       830       840
TCTGCACGGGTTCTGGATGGAATCCTCAGCCTTCCTGTGAAGAAATGACATGTTTGACTC   rFH4.3
-----------------------------------------------------------   rFH2.7
-----------------------------------------------------------   rFH1.8
-----------------------------------------------------------   rFH1.0


            850       860       870       880       890       900
CATATATTCCAAATGGTATCTACACACCTCACAGGATTAAACACAGAATTGATGATGAAA   rFH4.3
-----------------------------------------------------------   rFH2.7
-----------------------------------------------------------   rFH1.8
-----------------------------------------------------------   rFH1.0


            910       920       930       940       950       960
TCAGATATGAATGTAAAAATGGCTTCTATCCTGCAACCCGATCACCTGTTTCAAAGTGTA   rFH4.3
-----------------------------------------------------------   rFH2.7
-----------------------------------------------------------   rFH1.8
-----------------------------------------------------------   rFH1.0


                             SCR6
            970       980       990      1000      1010      1020
CAATTACTGGCTGGATCCCTGCTCCAAGATGTAGCTTGAAACCTTGTGATTTTCCACAAT   rFH4.3
-------------------------------------------TTGAAACCTTGTGATTTTCCACAAT   rFH2.7
-----------------------------------------------------------   rFH1.8
-----------------------------------------------------------   rFH1.0


           1030      1040      1050      1060      1070      1080
TCAAACATGGACGTCTGTATTATGAAGAAAGCCGGAGACCCTACTTCCCAGTACCTATAG   rFH4.3
TCAAACATGGACGTCTGTATTATGAAGAAAGCCGGAGACCCTACTTCCCAGTACCTATAG   rFH2.7
-----------------------------------------------------------   rFH1.8
-----------------------------------------------------------   rFH1.0
```

```
            1090      1100      1110      1120      1130      1140
GAAAGGAGTACAGCTATAACTGTGACAACGGGTTTACAACGCCTTCACAGTCATACTGGG    rFH4.3
GAAAGGAGTACAGCTATAACTGTGACAACGGGTTTACAACGCCTTCACAGTCATACTGGG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


                                                        SCR7
            1150      1160      1170      1180      1190      1200
ACTACCTTCGTTGCACAGTAAATGGGTGGGAGCCTGAAGTTCCATGCCTCAGGCAATGTA    rFH4.3
ACTACCTTCGTTGCACAGTAAATGGGTGGGAGCCTGAAGTTCCATGCCTCAGGCAATGTA    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1210      1220      1230      1240      1250      1260
TTTTCCATTATGTGGAATATGGAGAATCTTCATACTGGCAAAGAAGATATATAGAGGGTC    rFH4.3
TTTTCCATTATGTGGAATATGGAGAATCTTCATACTGGCAAAGAAGATATATAGAGGGTC    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1270      1280      1290      1300      1310      1320
AGTCTGCAAAAGTCCAGTGTCACAGTGGCTATAGTCTTCCAAATGGTCAAGATACATATT    rFH4.3
AGTCTGCAAAAGTCCAGTGTCACAGTGGCTATAGTCTTCCAAATGGTCAAGATACATATT    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0


                                                    SCR8
            1330      1340      1350      1360      1370      1380
ATTGTACAGAGAATGGCTGGTCCCCTCCTCCCAAATGCGTCCGTATCAAGACTTGTTCAG    rFH4.3
ATTGTACAGAGAATGGCTGGTCCCCTCCTCCCAAATGCGTCCGTATCAAGACTTGTTCAG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


            1390      1400      1410      1420      1430      1440
TATCAGATATAGAAATTGAAAATGGGTTTTTTTCTGAATCTGATTATACATATGCTCTAA    rFH4.3
TATCAGATATAGAAATTGAAAATGGGTTTTTTTCTGAATCTGATTATACATATGCTCTAA    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
              1450      1460      1470      1480      1490      1500
      ATAGAAAAACACGGTATAGATGTAAACAGGGATATGTAACAAATACCGGAGAAATATCAG    rFH4.3
      ATAGAAAAACACGGTATAGATGTAAACAGGGATATGTAACAAATACCGGAGAAATATCAG    rFH2.7
      ------------------------------------------------------------    rFH1.8
                                                                      rFH1.0
```

```
                                                          SCR9
              1510      1520      1530      1540      1550      1560
      GAATAATTACTTGTCTTCAAGATGGATGGTCACCTCGACCCTCATGCATTAAGTCTTGTG    rFH4.3
      GAATAATTACTTGTCTTCAAGATGGATGGTCACCTCGACCCTCATGCATTAAGTCTTGTG    rFH2.7
      ------------------------------------------------------------    rFH1.8
      ------------------------------------------------------------    rFH1.0
```

```
              1570      1580      1590      1600      1610      1620
      ATATGCCTGTATTTGAGAATTCTATGACTAAGAATAATAACACATGGTTTAAACTCAATG    rFH4.3
      ATATGCCTGTATTTGAGAATTCTATGACTAAGAATAATAACACATGGTTTAAACTCAATG    rFH2.7
      ------------------------------------------------------------    rFH1.8
      ------------------------------------------------------------    rFH1.0
```

```
              1630      1640      1650      1660      1670      1680
      ACAAATTAGACTATGAATGTCACATTGGATATGAAAATGAATATAAACATACCAAAGGCT    rFH4.3
      ACAAATTAGACTATGAATGTCACATTGGATATGAAAATGAATATAAACATACCAAAGGCT    rFH2.7
      ------------------------------------------------------------    rFH1.8
      ------------------------------------------------------------    rFH1.0
```

```
                                                          SCR10
              1690      1700      1710      1720      1730      1740
      CTATAACATGTACTTATGATGGATGGTCTAGTACACCCTCCTGTTATGAAAGAGAATGCA    rFH4.3
      CTATAACATGTACTTATGATGGATGGTCTAGTACACCCTCCTGTTATGAAAGAGAATGCA    rFH2.7
      ------------------------------------------------------------    rFH1.8
      ------------------------------------------------------------    rFH1.0
```

```
              1750      1760      1770      1780      1790      1800
      GCATTCCCCTGTTACACCAAGACTTAGTTGTTTTTCCCAGAGAAGTAAAATACAAAGTTG    rFH4.3
      GCATTCCCCTGTTACACCAAGACTTAGTTGTTTTTCCCAGAGAAGTAAAATACAAAGTTG    rFH2.7
      ------------------------------------------------------------    rFH1.8
      ------------------------------------------------------------    rFH1.0
```

```
        1810       1820       1830       1840       1850       1860
GAGATTCGTTGAGTTTCTCTTGCCGTTCAGGACACAGAGTTGGAGCAGATTTAGTGCAAT    rFH4.3
GAGATTCGTTGAGTTTCTCTTGCCGTTCAGGACACAGAGTTGGAGCAGATTTAGTGCAAT    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


                                                  SCR11
        1870       1880       1890       1900       1910       1920
GCTACCACTTTGGATGGTCCCCTAATTTCCCAACGTGTGAAGGCCAAGTAAAATCATGTG    rFH4.3
GCTACCACTTTGGATGGTCCCCTAATTTCCCAACGTGTGAAGGCCAAGTAAAATCATGTG    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0


        1930       1940       1950       1960       1970       1980
ACCAACCTCTTGAAATCCCGAATGGGGAAATAAAGGGAACAAAAAAAGTTGAATACAGCC    rFH4.3
ACCAACCTCTTGAAATCCCGAATGGGGAAATAAAGGGAACAAAAAAAGTTGAATACAGCC    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0


        1990       2000       2010       2020       2030       2040
ATGGTGACGTGGTGGAATATGATTGCAAACCTAGATTTCTACTGAAGGGACCCAATAAAA    rFH4.3
ATGGTGACGTGGTGGAATATGATTGCAAACCTAGATTTCTACTGAAGGGACCCAATAAAA    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0


                                                  SCR12
        2050       2060       2070       2080       2090       2100
TCCAGTGTGTTGACGGGAAGTGGACAAGGTTGCCGATATGCGTTGAGTATGAGAGAACAT    rFH4.3
TCCAGTGTGTTGACGGGAAGTGGACAAGGTTGCCGATATGCGTTGAGTATGAGAGAACAT    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0


        2110       2120       2130       2140       2150       2160
GTGGAGACCTTCCTGAACTTGAGCATGGCTCTGTCAAGTTATCTGTCCCTCCCTACCATC    rFH4.3
GTGGAGACCTTCCTGAACTTGAGCATGGCTCTGTCAAGTTATCTGTCCCTCCCTACCATC    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0
```

```
          2170      2180      2190      2200      2210      2220
ATGGAGATTCAGTGGAGTTCACTTGTACAGAAACCTTCACAATGATTGGACATGCAGTAG    rFH4.3
ATGGAGATTCAGTGGAGTTCACTTGTACAGAAACCTTCACAATGATTGGACATGCAGTAG    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0


                                                   SCR13
          2230      2240      2250      2260      2270      2280
TTTTCTGCATTAGTGGAAGGTGGACCGAGCTTCCTCAATGTGTTGCAACAGATCAACTGG    rFH4.3
TTTTCTGCATTAGTGGAAGGTGGACCGAGCTTCCTCAATGTGTTGCAACAGATCAACTGG    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0


          2290      2300      2310      2320      2330      2340
AGAAGTGTAAAGCCCCGAAGTCAACTGGCATAGATGCAATTCATCCAAATAAGAATGAAT    rFH4.3
AGAAGTGTAAAGCCCCGAAGTCAACTGGCATAGATGCAATTCATCCAAATAAGAATGAAT    rFH2.7
----------------------------------------------------------    rFH1.8
                                                               rFH1.0


          2350      2360      2370      2380      2390      2400
TTAATCATAACTTTAGTGTGAGTTACAGATGTAGACAAAAGCAGGAGTATGAACATTCAA    rFH4.3
TTAATCATAACTTTAGTGTGAGTTACAGATGTAGACAAAAGCAGGAGTATGAACATTCAA    rFH2.7
----------------------------------------------------------    rFH1.8
----------------------------------------------------------    rFH1.0


                         SCR14
          2410      2420      2430      2440      2450      2460
TCTGCATCAATGGAAGATGGGATCCTGAACCAAACTGTACAAGCAAAAGATTCTGCCCTC    rFH4.3
TCTGCATCAATGGAAGATGGGATCCTGAACCAAACTGTACAAGCAAAAGATTCTGCCCTC    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0


          2470      2480      2490      2500      2510      2520
CTCCCCCGCAGATTCCAAATGCCCAAGTGATTGAAACCACCGTGAAATACTTGGATGGAG    rFH4.3
CTCCCCCGCAGATTCCAAATGCCCAAGTGATTGAAACCACCGTGAAATACTTGGATGGAG    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0
```

```
              2530      2540      2550      2560      2570      2580
AAAAAGTATCTGTTCTTTGCCAAGATGGTTACCTAACTCAGGGCCCAGAAGAAATGGTGT    rFH1.8
AAAAAGTATCTGTTCTTTGCCAAGATGGTTACCTAACTCAGGGCCCAGAAGAAATGGTGT    rFH2.7
-----------------------------------------------------------    rFH4.3
-----------------------------------------------------------    rFH1.0
```

```
                                                  SCR15
              2590      2600      2610      2620      2630      2640
GTAAACATGGAAGGTGGCAGTCGTTACCACGCTGCACGGAAAAAAATTCCATGTTCCCAGC    rFH4.3
GTAAACATGGAAGGTGGCAGTCGTTACCACGCTGCACGGAAAAAAATTCCATGTTCCCAGC    rFH2.7
------------------------------------------------------------    rFH1.8
------------------------------------------------------------    rFH1.0
```

```
              2650      2660      2670      2680      2690      2700
CCCCTAAAATTGAACATGGATCTATTAAGTCGCCCAGGTCCTCAGAAGAGAGGAGAGATT    rFH4.3
CCCCTAAAATTGAACATGGATCTATTAAGTCGCCCAGGTCCTCAGAAGAGAGGAGAGATT    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0
```

```
              2710      2720      2730      2740      2750      2760
TAATTGAGTCCAGCAGTTATGAACACGGAACTACATTCAGCTATTGCTGTAGAGATGGAT    rFH4.3
TAATTGAGTCCAGCAGTTATGAACACGGAACTACATTCAGCTATTGCTGTAGAGATGGAT    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0
```

```
              2770      2780      2790      2800      2810      2820
TCAAGATATCTGAAGAAAATAGGGTAACCTGCAACATGGGAAAATGGAGCTCTCTGCCTC    rFH4.3
TCAAGATATCTGAAGAAAATAGGGTAACCTGCAACATGGGAAAATGGAGCTCTCTGCCTC    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0
```

```
        SCR16
              2830      2840      2850      2860      2870      2880
GTTGTGTTGGAATACCTTGTGGACCCCCACCTTCAATTCCTCTTGGTATTGTTTCTCATG    rFH4.3
GTTGTGTTGGAATACCTTGTGGACCCCCACCTTCAATTCCTCTTGGTATTGTTTCTCATG    rFH2.7
-----------------------------------------------------------    rFH1.8
-----------------------------------------------------------    rFH1.0
```

```
              2890       2900       2910       2920       2930       2940
AACTAGAAAGTTACCAATATGGAGAGGAGGTTACATACAATTGTTCTGAAGGCTTTGGAA  rFH4.3
AACTAGAAAGTTACCAATATGGAGAGGAGGTTACATACAATTGTTCTGAAGGCTTTGGAA  rFH2.7
------------------------------------------------------------  rFH1.8
------------------------------------------------------------  rFH1.0


              2950       2960       2970       2980       2990       3000
TTGATGGACCAGCATTTATTAAATGTGTAGGAGGACAGTGGTCTGAACCTCCCAAATGCA  rFH4.3
TTGATGGACCAGCATTTATTAAATGTGTAGGAGGACAGTGGTCTGAACCTCCCAAATGCA  rFH2.7
------------------------------------------------------------  rFH1.8
------------------------------------------------------------  rFH1.0


     SCR17
              3010       3020       3030       3040       3050       3060
TAAAAACTGATTGTGACAACTTGCCCACATTTGAAATTGCCAAACCGACAGAAAAGAAAA  rFH4.3
TAAAAACTGATTGTGACAACTTGCCCACATTTGAAATTGCCAAACCGACAGAAAAGAAAA  rFH2.7
------------------------------------------------------------  rFH1.8
------------------------------------------------------------  rFH1.0


              3070       3080       3090       3100       3110       3120
AAAAATCATACAGGTCAGGAGAACAAGTGACATTCAGATGTCCACCTCCGTATCGAATGG  rFH4.3
------------------------------------------------------------  rFH2.7
-----------------------------------------------TATCGAATGG  rFH1.8
------------------------------------------------------------  rFH1.0


              3130       3140       3150       3160       3170       3180
ATGGCTCTGACATTGTCACATGTGTTAATACGAAGTGGATTGGACAGCCGGTATGCAAAG  rFH4.3
------------------------------------------------------------  rFH2.7
ATGGCTCTGACATTGTCACATGTGTTAATACGAAGTGGATTGGACAGCCGGTATGCAAAG  rFH1.8
------------------------------------------------------------  rFH1.0


     SCR18
              3190       3200       3210       3220       3223       3240
ATAATTCCTGTGTGAATCCACCACATGTGCCAAATGCTACTATACTAACAAGGCACAAGA  rFH4.3
------------------------------------------------------------  rFH2.7
ATAATTCCTGTGTGAATCCACCACATGTGCCAAATGCTACTATACTAACAAGGCACAAGA  rFH1.8
------------------------------------------------------------  rFH1.0
```

```
               3250      3260      3270      3280      3290      3300
CTAAATATCCATCTGGTGACAAAGTACGTTATGACTGTAATAAACCTTTTGAATTATTTG   rFH4.3
------------------------------------------------------------   rFH2.7
CTAAATATCCATCTGGTGACAAAGTACGTTATGACTGTAATAAACCTTTTGAATTATTTG   rFH1.8
------------------------------------------------------------   rFH1.0
```

```
               3310      3320      3330      3340      3350      3360
GGGAAGTGGAAGTGATGTGCCAAAACGGGATTTGGACAGAACCACCGAAATGCAAAGATT   rFH4.3
------------------------------------------------------------   rFH2.7
GGGAAGTGGAAGTGATGTGCCAAAACGGGATTTGGACAGAACCACCGAAATGCAAAGATT   rFH1.8
------------------------------------------------------------   rFH1.0
```

```
 SCR19
               3370      3380      3390      3400      3410      3420
CAACAGGGAAATGTGGGCCTCCTCCACCTATTGACAATGGAGACATCACCTCCTTGTCAT   rFH4.3
------------------------------------------------------------   rFH2.7
CAACAGGGAAATGTGGGCCTCCTCCACCTATTGACAATGGAGACATCACCTCCTTGTCAT   rFH1.8
------------------------------------------------------------   rFH1.0
```

```
               3430      3440      3450      3460      3470      3480
TACCAGTATATGCACCATTATCATCAGTTGAATATCAATGCCAGAACTATTATCTACTTA   rFH4.3
------------------------------------------------------------   rFH2.7
TACCAGTATATGCACCATTATCATCAGTTGAATATCAATGCCAGAACTATTATCTACTTA   rFH1.8
------------------------------------------------------------   rFH1.0
```

```
               3490      3500      3510      3520      3530      3540
AGGGAAATAAGATAGTAACATGTAGAAATGGAAAGTGGTCTCAGCCACCAACCTGCTTAC   rFH4.3
------------------------------------------------------------   rFH2.7
AGGGAAATAAGATAGTAACATGTAGAAATGGAAAGTGGTCTCAGCCACCAACCTGCTTAC   rFH1.8
------------------------------------------------------------   rFH1.0
```

```
 SCR20
               3550      3560      3570      3580      3590      3600
ATGCATGTGTGATACCAGAAGATATTATGGAAAAACATAATATAGTTCTCAGATGGAGGG   rFH4.3
------------------------------------------------------------   rFH2.7
ATGCATGTGTGATACCAGAAGATATTATGGAAAAACATAATATAGTTCTCAGATGGAGGG   rFH1.8
------------------------------------------------------------   rFH1.0
```

```
          3610      3620      3630      3640      3650      3660
AAAATGCAAAGATTTATTCCCAATCAGGGGAGAATATTGAATTCATGTGTAAACCTGGAT   rFH4.3
-----------------------------------------------------------   rFH2.7
AAAATGCAAAGATTTATTCCCAATCAGGGGAGAATATTGAATTCATGTGTAAACCTGGAT   rFH1.8
--------------------------------------------------------GGAT   rFH1.0


          3670      3680      3690      3700      3710      3720
ATAGAAAATTCAGAGGATCACCTCCGTTTCGTACAAAGTGCATTGAGGGTCACATCAATT   rFH4.3
-----------------------------------------------------------   rFH2.7
ATAGAAAATTCAGAGGATCACCTCCGTTTCGTACAAAGTGCATTGAGGGTCACATCAATT   rFH1.8
ATAGAAAATTCAGAGGATCACCTCCGTTTCGTACAAAGTGCATTGAGGGTCACATCAATT   rFH1.0


          3730      3740      3750      3760      3770      3780
ATCCCACTTGTGTATAAaatcgctatacaattattagtaaaccttatggatgagaaatgc   rFH4.3
-----------------------------------------------------------   rFH2.7
ATCCCACTTGTGTATAAaatcgctatacaattattagtaaaccttatggatgagaaatgc   rFH1.8
ATCCCACTTGTGTATAAaatcgctatacaattattagtaaaccttatggatgacactttg   rFH1.0


          3790      3800      3810      3820      3830      3840
acatgtatattactaatacagtttgaatttacatttaaatattgtttagctcatttcctc   rFH4.3
-----------------------------------------------------------   rFH2.7
acatgtatattactaatacagtttgaatttacatttaaatattgtttagctcatttcctc   rFH1.8
tttagaaatgcacatgtatattactaatacagtttgaatttacatttgaaaaa-------   rFH1.0


          3850      3860      3870      3880      3890      3900
taataagtatataaactttttttatatggtggttaatcagtaactttacagactgttgcc   rFH4.3
-----------------------------------------------------------   rFH2.7
taataagtatataaactttttttatatggtggttaatcagtaactttacagactgttgcc   rFH1.8
-----------------------------------------------------------   rFH1.0
```

```
            3910       3920       3930       3940       3950       3960
acaaagcaagaacattacattcaaaactcctaatccaaatatgatatgtccaaggacaaa    rFH4.3
-------------------------------------------------------------    rFH2.7
acaaagcaagaacattacattcaaaactcctaatccaaatatgatatgtccaaggacaaa    rFH1.8
-------------------------------------------------------------    rFH1.0



            3970       3980       3990       4000       4010       4020
ctatgtctaagcaagaaaataaatgttagttcttcaatgtctgttttttattcaggacctt    rFH4.3
-------------------------------------------------------------    rFH2.7
ctatgtctaagcaagaaaataaatgttagttcttcaatgtctgttttttattcaggacctt    rFH1.8
-------------------------------------------------------------    rFH1.0



            4030       4040       4050       4060       4070       4080
tcagatttttcttggataccttttgttaggttctgattcacagtgagtggaagacacactg    rFH4.3
-------------------------------------------------------------    rFH2.7
tcagatttttcttggataccttttgttaggttctgattcacagtgagtggaagacacactg    rFH1.8
-------------------------------------------------------------    rFH1.0



            4090       4100       4110       4120       4130       4140
actctgacttcaaattagtattacttgcaatacattaacaaccaaactatcataatatca    rFH4.3
-------------------------------------------------------------    rFH2.7
actctgacttcaaattagtattacttgcaatacattaacaaccaaactatcataatatca    rFH1.8
-------------------------------------------------------------    rFH1.0



            4150       4160       4170       4180       4190       4200
caaatgtatacagctaattactgtgtcctacctttgtatcaataaagaaatctaagaaag    rFH4.3
-------------------------------------------------------------    rFH2.7
caaatgtatacagctaattactgtgtcctacctttgtatcaataaagaaatctaagaaag    rFH1.8
-------------------------------------------------------------    rFH1.0



            4210       4220       4230
ttcttgcttaaaaaaaaaaaaaaaaaaaaa                                  rFH4.3
------------------------------                                  rFH2.7
ttcttgcttaaaaaaaaaaaaaaaaaaaaa                                  rFH1.8
------------------------------                                  rFH1.0
```